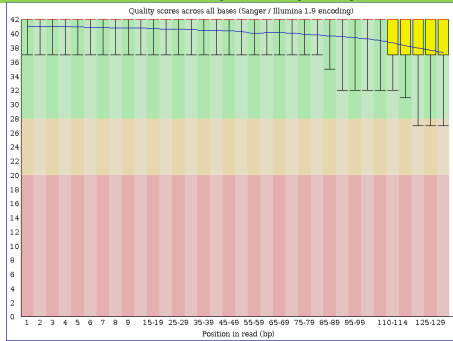


Supplementary figure 1: Fast QC (quality control) data

| Goat ID | Basic statistics | | Goat ID | Basic statistics | |
|---------|--------------------|-------------------------|---------|--------------------|-------------------------|
| X18 | Measure | Value | A101 | Measure | Value |
| | Filename | 18_1.paired.fq | | Filename | A101_1.paired.fq |
| | File type | Conventional base calls | | File type | Conventional base calls |
| | Encoding | Sanger / Illumina 1.9 | | Encoding | Sanger / Illumina 1.9 |
| | Total Sequences | 18344612 | | Total Sequences | 22740578 |
| | Filtered Sequences | 0 | | Filtered Sequences | 0 |
| | Sequence length | 50-130 | | Sequence length | 50-105 |
| | %GC | 52 | | %GC | 55 |
| A002 | Measure | Value | X066 | Measure | Value |
| | Filename | A002_1.paired.fq | | Filename | 066_1.paired.fq |
| | File type | Conventional base calls | | File type | Conventional base calls |
| | Encoding | Sanger / Illumina 1.9 | | Encoding | Sanger / Illumina 1.9 |
| | Total Sequences | 20611561 | | Total Sequences | 22153023 |
| | Filtered Sequences | 0 | | Filtered Sequences | 0 |
| | Sequence length | 50-130 | | Sequence length | 50-105 |
| | %GC | 51 | | %GC | 52 |
| H095 | Measure | Value | X043 | Measure | Value |
| | Filename | H096_1.paired.fq | | Filename | 043_1.paired.fq |
| | File type | Conventional base calls | | File type | Conventional base calls |
| | Encoding | Sanger / Illumina 1.9 | | Encoding | Sanger / Illumina 1.9 |
| | Total Sequences | 19275680 | | Total Sequences | 25440163 |
| | Filtered Sequences | 0 | | Filtered Sequences | 0 |
| | Sequence length | 50-130 | | Sequence length | 50-105 |
| | %GC | 51 | | %GC | 50 |
| X248 | Measure | Value | B15 | Measure | Value |
| | Filename | 248_1.paired.fq | | Filename | B15_1.paired.fq |
| | File type | Conventional base calls | | File type | Conventional base calls |
| | Encoding | Sanger / Illumina 1.9 | | Encoding | Sanger / Illumina 1.9 |
| | Total Sequences | 22221239 | | Total Sequences | 25789160 |
| | Filtered Sequences | 0 | | Filtered Sequences | 0 |
| | Sequence length | 50-130 | | Sequence length | 50-105 |
| | %GC | 51 | | %GC | 50 |

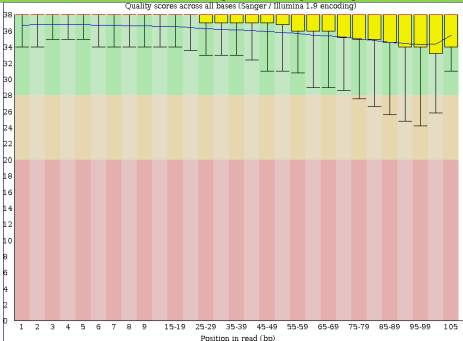
Goat ID
X18

Per base sequence quality

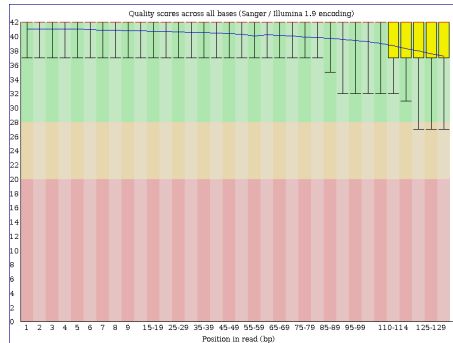


Goat ID
A101

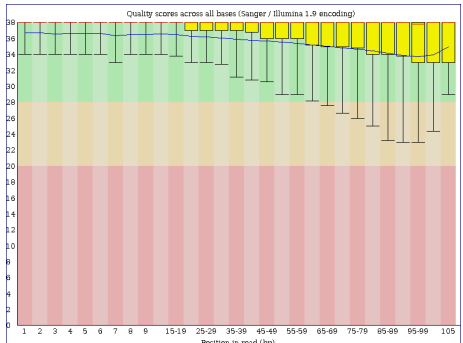
Per base sequence quality



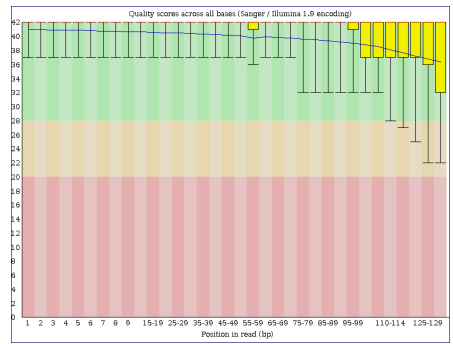
A002



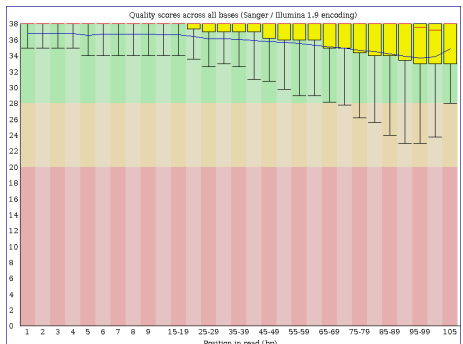
X066



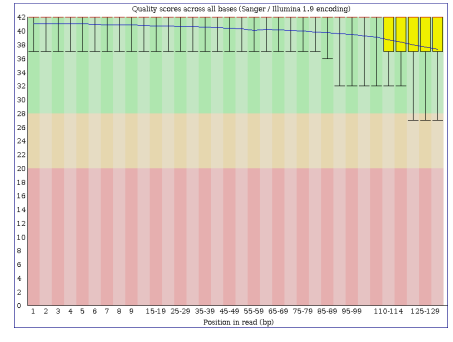
H095



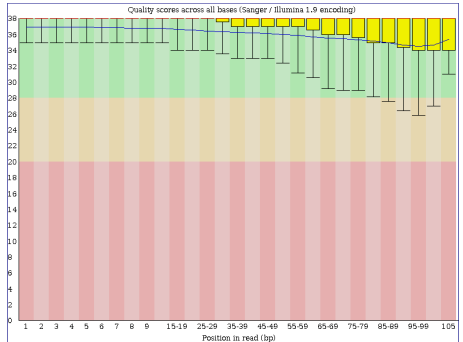
X043



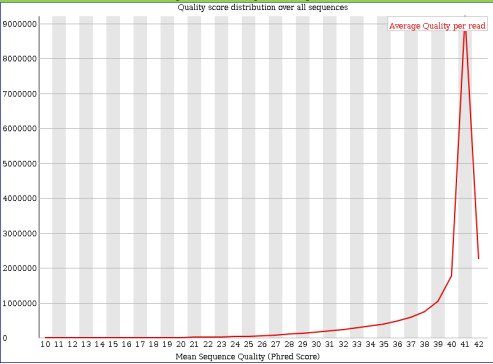
X248



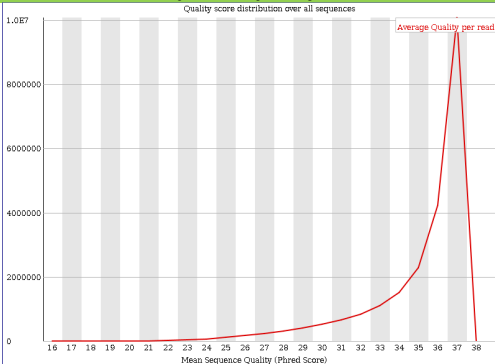
B15



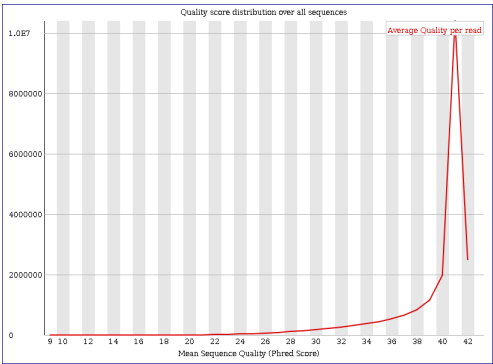
Goat ID **X18** Per sequence quality scores



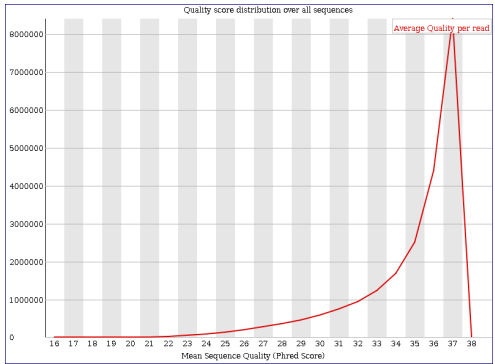
Goat ID **A101** Per sequence quality scores



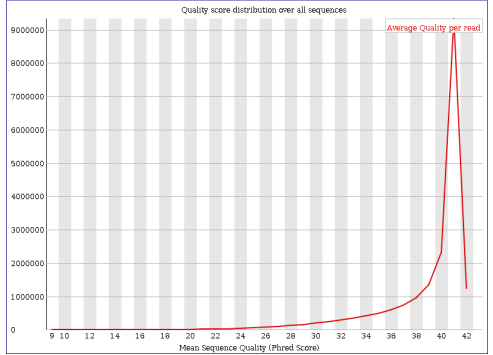
A002



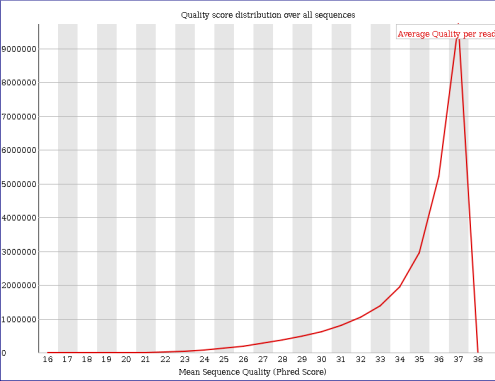
X066



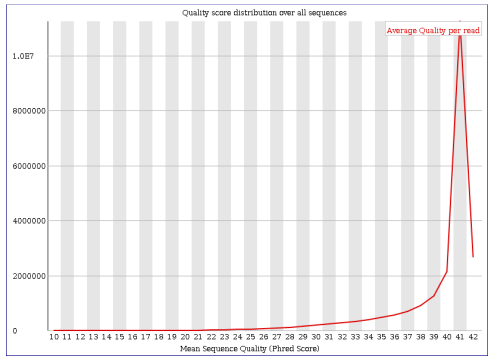
H095



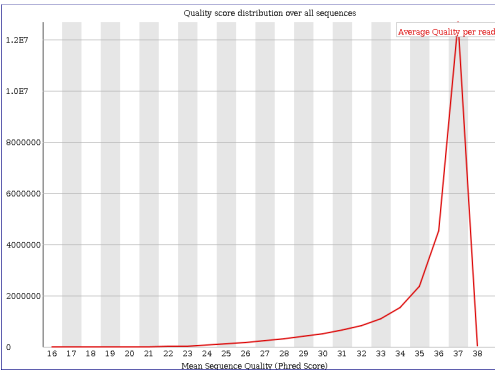
X043



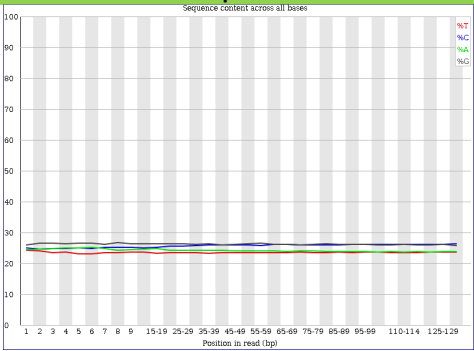
X248



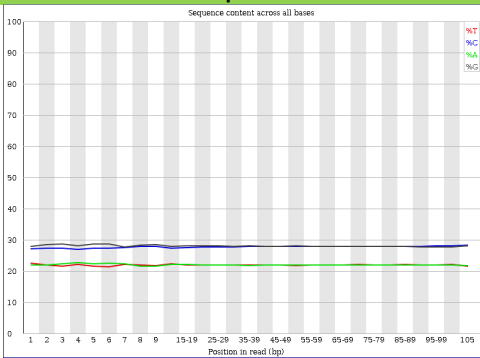
B15



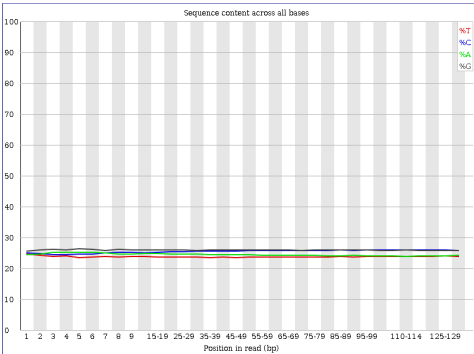
Goat ID
X18



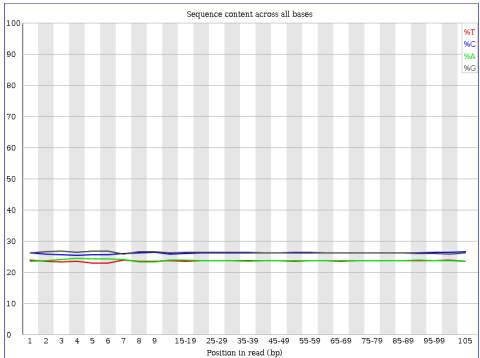
Goat ID
A101



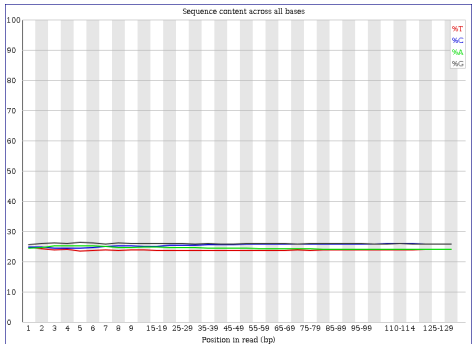
A002



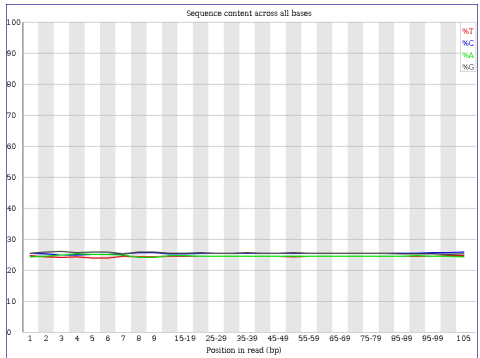
X066



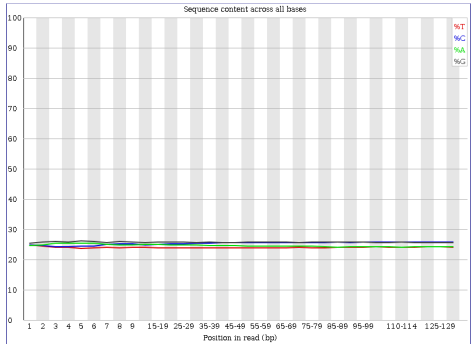
H095



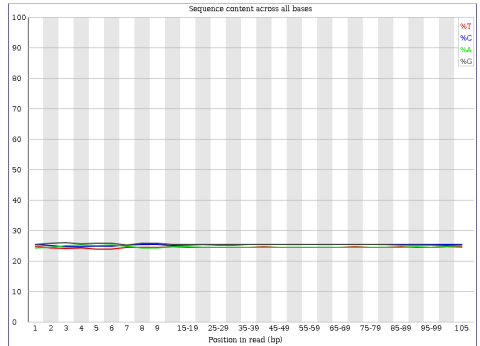
X043



X248

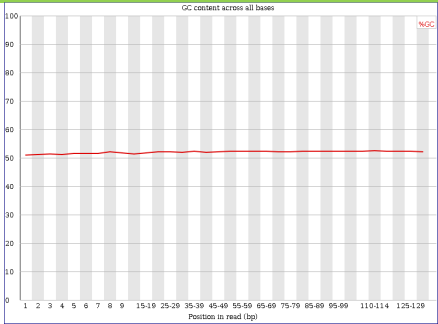


B15



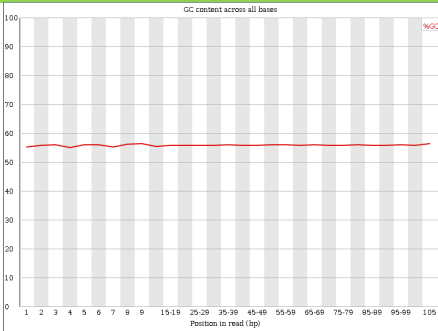
Goat ID
X18

Per base GC content

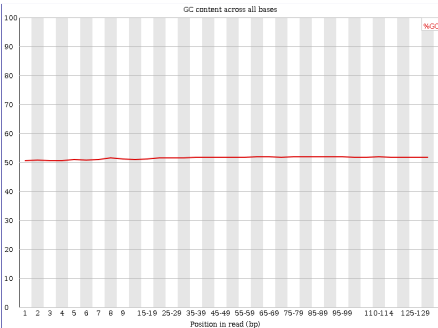


Goat ID
A101

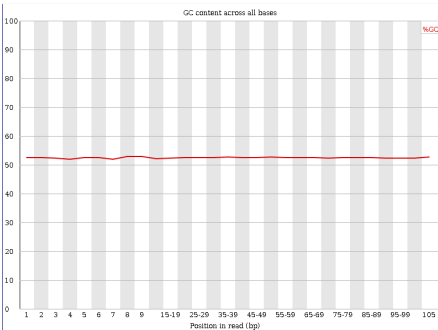
Per base GC content



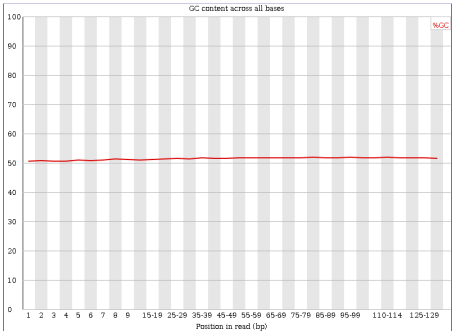
A002



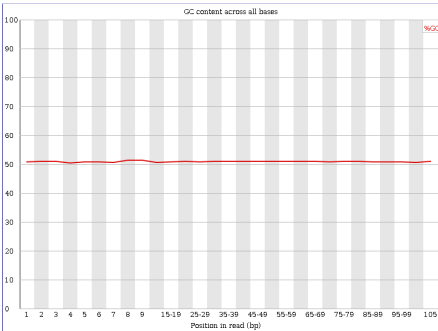
X066



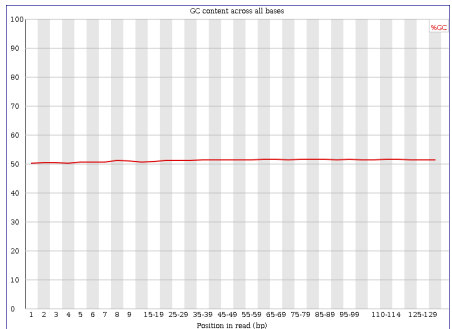
H095



X043



X248



B15

